

SEQUENCE LISTING

<110> Brett P. Monia
Kenneth W. Dobie

<120> ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION

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ctctcccggc cgagccgcgg cggcagcagc agcagcagca gcagcaggag gaggagcccg 180

gtggcggcgg tggccgggga gccc atg gcg tac agt caa gga ggc ggc aaa 231

Met Ala Tyr Ser Gln Gly Gly Gly Lys

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aaa aaa gtc tgc tac tac tac gac ggt gat att gga aat tat tat tat 279

Lys Lys Val Cys Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr

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gga cag ggt cat ccc atg aag cct cat aga atc cgc atg acc cat aac 327

Gly Gln Gly His Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn

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ttg ctg tta aat tat ggc tta tac aga aaa atg gaa ata tat agg ccc 375

Leu Leu Leu Asn Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro

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cat aaa gcc act gcc gaa gaa atg aca aaa tat cac agt gat gag tat 423

His Lys Ala Thr Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr

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atc aaa ttt cta cgg tca ata aga cca gat aac atg tct gag tat agt	471
Ile Lys Phe Leu Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser	
75 80 85	
aag cag atg cat ata ttt aat gtt gga gaa gat tgt cca gcg ttt gat	519
Lys Gln Met His Ile Phe Asn Val Gly Glu Asp Cys Pro Ala Phe Asp	
90 95 100 105	
gga ctc ttt gag ttt tgt cag ctc tca act ggc ggt tca gtt gct gga	567
Gly Leu Phe Glu Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly	
110 115 120	
gct gtg aag tta aac cga caa cag act gat atg gct gtt aat tgg gct	615
Ala Val Lys Leu Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala	
125 130 135	
gga gga tta cat cat gct aag aaa tac gaa gca tca gga ttc tgt tac	663
Gly Gly Leu His His Ala Lys Lys Tyr Glu Ala Ser Gly Phe Cys Tyr	
140 145 150	
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Val Asn Asp Ile Val Leu Ala Ile Leu Glu Leu Lys Tyr His Gln	
155 160 165	
aga gtc tta tat att gat ata gat att cat cat ggt gat ggt gtt gaa	759
Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu	
170 175 180 185	
gaa gct ttt tat aca aca gat cgt gta atg acg gta tca ttc cat aaa	807
Glu Ala Phe Tyr Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys	
190 195 200	
tat ggg gaa tac ttt cct ggc aca gga gac ttg agg gat att ggt gct	855
Tyr Gly Glu Tyr Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala	
205 210 215	
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Gly Lys Gly Lys Tyr Tyr Ala Val Asn Phe Pro Met Cys Asp Gly Ile	
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Asp Asp Glu Ser Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val	
235 240 245	
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Met Glu Met Tyr Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp	
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Ser Leu Ser Gly Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly	
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His Ala Lys Cys Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu	
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Met Leu Gly Gly Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp	
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aca tat gag act gca gtt gcc ctt gat tgt gag att ccc aat gag ttg	1191
Thr Tyr Glu Thr Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu	
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cca tat aat gat tac ttt gag tat ttt gga cca gac ttc aaa ctg cat	1239
Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His	
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Ile Ser Pro Ser Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu	
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aag ata aaa cag cgt ttg ttt gaa aat ttg cgc atg tta cct cat gca	1335
Lys Ile Lys Gln Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala	
365	370 375
cct ggt gtc cag atg caa gct att cca gaa gat gct gtt cat gaa gac	1383
Pro Gly Val Gln Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp	
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agt gga gat gaa gat gga gaa gat cca gac aag aga att tct att cga	1431
Ser Gly Asp Glu Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg	
395	400 405
gca tca gac aag cgg ata gct tgt gat gaa gaa ttc tca gat tct gag	1479
Ala Ser Asp Lys Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu	
410	415 420 425
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Asp Glu Gly Glu Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly	

430	435	440	
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Ala Lys Lys Ala Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys			
445	450	455	
aaa aca gac gtt aag gaa gaa gat aaa tcc aag gac aac agt ggt gaa			1623
Lys Thr Asp Val Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu			
460	465	470	
aaa aca gat acc aaa gga acc aaa tca gaa cag ctc agc aac ccc tga			1671
Lys Thr Asp Thr Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro			
475	480	485	
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tcaaattggga ctttttcggt tttgtttttc tgggcaagtt ttattgtgag attttcta			1851
tatgaagcaa aattttctttt ctccaccatg ctttatgtga tagtatttaa aattgatgtg			1911
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PTS-0022

-22-

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